

Fig. 1A

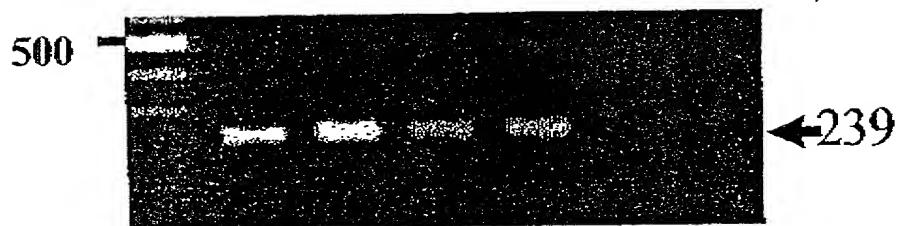


Fig. 1B



Fig. 1C

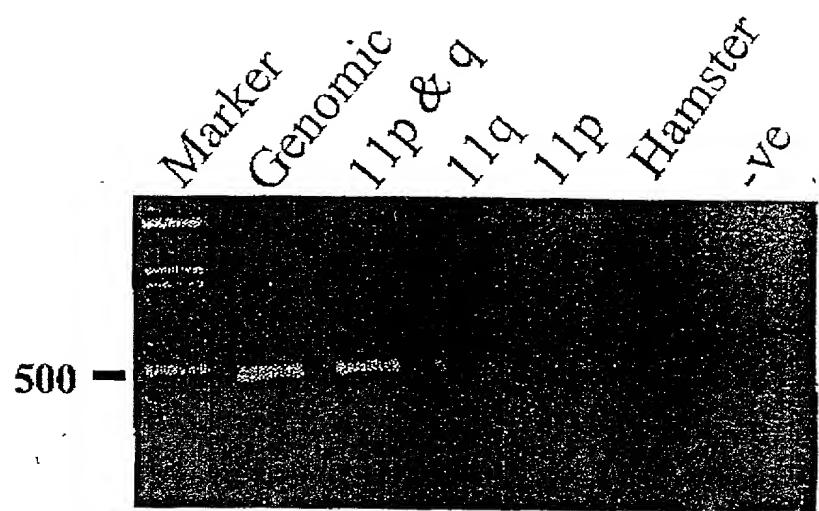


Fig. 2

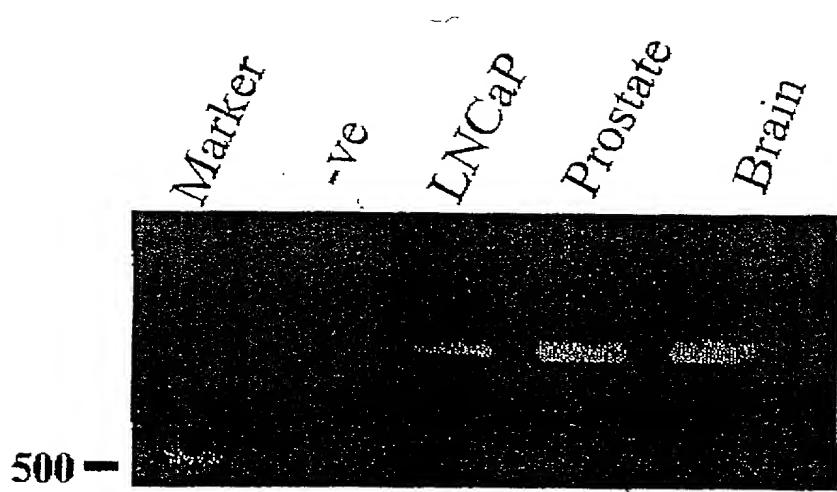


Fig. 3

PSMA	1	MWNLLHETDSAVALARRPRWLCA	40
		AGALVLAGGFFLLGFLFG	0
PSMA-LIKE	1		
	41	WFIKSSNEATNITPKHNMKAFLDELKAENIKKFLYNFTQI	80
	1		0
	81	PHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYP	120
	1		0
	121	NKTHPNYISIINEDGNEIFNTSLFEP	160
	1	PPPPPGYENVSDIVPP	0
	161	FSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINC	200
	1	SGKI	0
	201	VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVK	240
	1		0
	241	SYPDGWNLPGGVQRGNILNLNGAGDPLTPGYPANEYAYR	280
	1		0
	281	RGIAEAVGLPSIPVHPIGYYDAQKLLEK	320
	1	MGGSGAPPDSSWR	12

	321	GSLKVPYNVGP	360
	13	GFTGNFSTQKV	52

	361	KGHRDSVFGGIDPQSGAAVVHEIVR	400
	53	TLRGAVEPDYVILGGHRDSVFGGIDPQSGAAVVHETVR	92
		*****	**

Fig. 4-1

401 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEE NSR 440
93 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAED NSR 132

441 LLQERGVAYINADSSIEGNYTLRVDCPLMYSLVHNL TKE 480
133 LLQERGVAYINADSSIEGNYTLRVDCPLMYSLVYNLTKE 172

481 LKSPDEGFEGKSLYESWTKSPSPEFGMPRISKLGSGND 520
173 LKSPDEGFEGKSLYESWTKSPSPEFGMPRISKLGSGND 212

521 FEVFFQRLGIASGRARYTKNWETNKFGYPLYHSVYETYE 560
213 FEVFFQRLGIASGRARYTKNWETNKFGYPLYHSVYETYE 252

561 LVEKFYDPMFKYH LTVAQVRGGMVFELANSIVLPFDCRDY 600
253 LVEKFYDPMFKYH LTVAQVRGGMVFELANSIVLPFDCRDY 292

601 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFT 640
293 AVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFT 332

641 EIASKFSERLQDFDKSNPIVLRMMNDQLMFLERA FIDPLG 680
333 EIASKFSERLQDFDKSNPII LRMMNDQLMFLERA FIDPLG 372

681 LPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 720
373 LPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 412

721 PSKAWGEVKRQIYVAAFTVQAAAETLSEVA (SEQ ID NO: 4)
413 PSKAWGDVKRQISVAAFTVQAAAETLSEVA (SEQ ID NO: 2)

Fig. 4-2

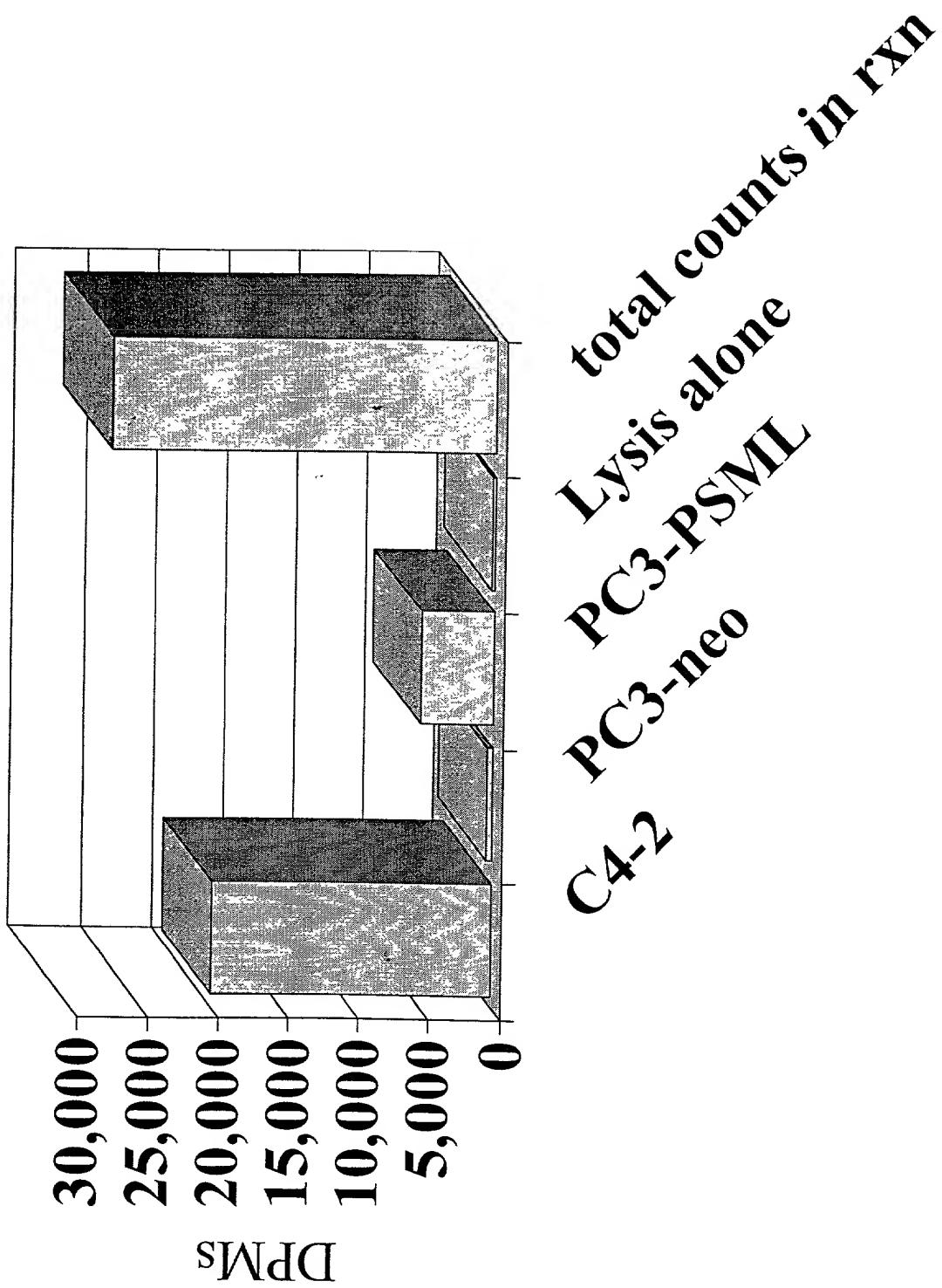


FIG. 5

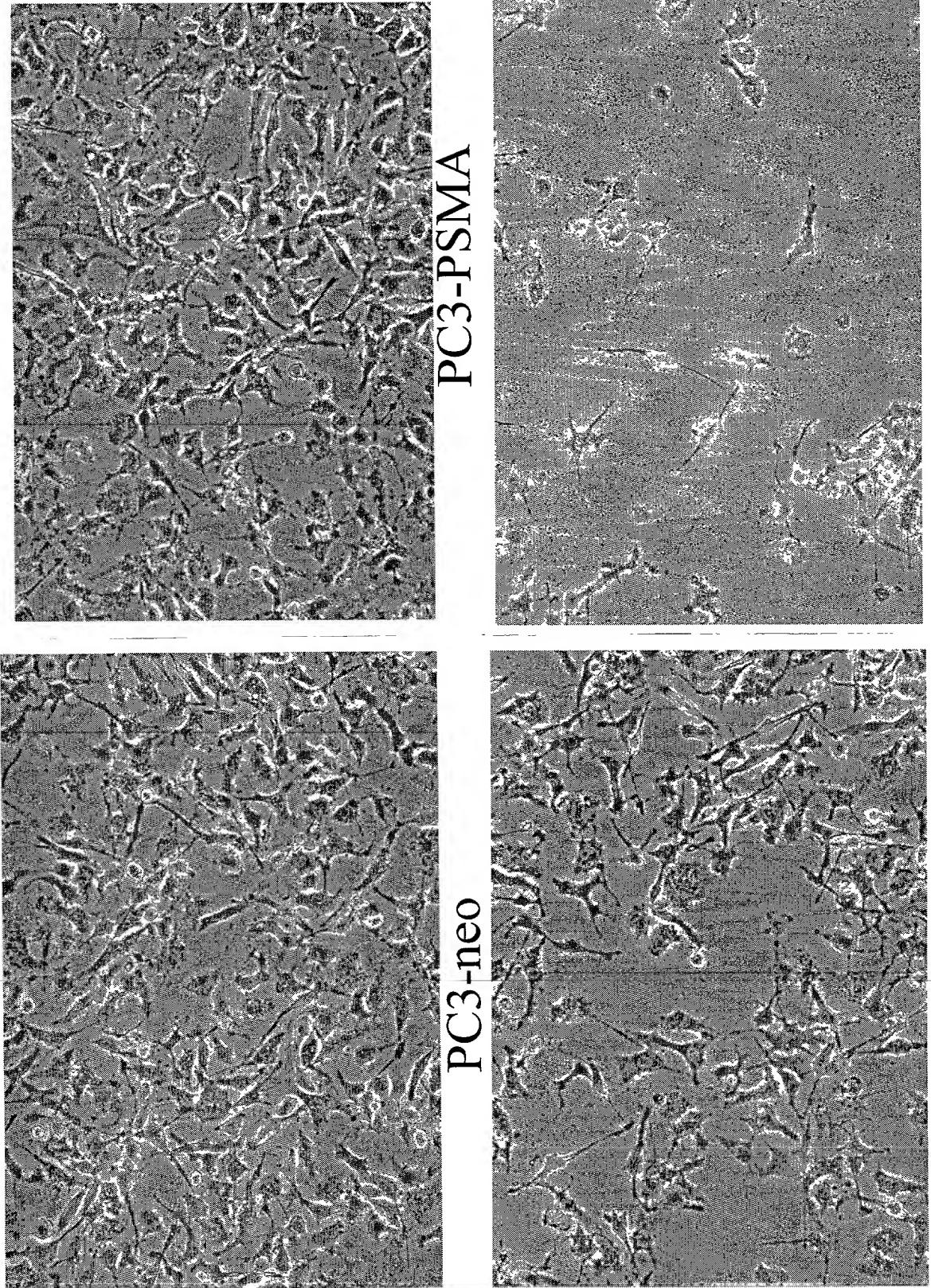


Fig. 6